

> O <
O||O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seqid2_vs_4and6.res made by spaul on Fri 19 Mar 104 13:49:58-PST.

Query sequence being compared: US-09-982-828-2 (1-1863)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-982-828-2 (1-1863) with:
File: US09982828.pep

100-

N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
E 5-
Q -
U -
E -
N -
C -
E -
S 0

SCORE 0 207 414 621 828 1035 1242 1449 1656 1863
STDEV

PARAMETERS

Similarity matrix PAM-150 K-tuple 2
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 500
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 1862 Median 1863 Standard Deviation 0.58
Times: CPU 00:00:00.01 Total Elapsed 00:00:00.00

Number of residues: 5589
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

Sequence Name Description Length Score Score Init. Opt. Sig. Frame

1. US-09-982-828-4 Sequence 4, Application US 1863 1863 1863 1.73 0
2. US-09-982-828-2 Sequence 2, Application US 1863 1863 1863 1.73 0

The list of other best scores is:

Sequence Name Description Length Score Score Init. Opt. Sig. Frame
3. US-09-982-828-6 Sequence 6, Application US 1863 1862 1862 0.00 0

1. US-09-982-828-2 (1-1863)
US-09-982-828-4 Sequence 4, Application US/09982828

Initial Score = 1863 Optimized Score = 1863 Significance = 1.73
Residue Identity = 100% Matches = 1863 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
MDLSALRVEEYQNVINAMOKILEPCICLELIKEPVSTKCDHIFCKFCMLKLLNOKKGPSQCLCKNDITKRS
MDLSALRVEEYQNVINAMOKILEPCICLELIKEPVSTKCDHIFCKFCMLKLLNOKKGPSQCLCKNDITKRS
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
LQESTRFSOLVEELLKIIICAFQDGTGLEIYANSYFPAKKNNSPEHLKDEVIIOISMGYRNRAKRLLOSEPEN
LQESTRFSOLVEELLKIIICAFQDGTGLEIYANSYFPAKKNNSPEHLKDEVIIOISMGYRNRAKRLLOSEPEN
80 90 100 110 120 130 140

150 160 170 180 190 200 210
PSLQETSLSVOLSNLGTVRTLTKRQIOPQKTSVYIELGSDSSDVTNKAATYCSVGDQELLIQITPQGRDEI
PSLQETSLSVOLSNLGTVRTLTKRQIOPQKTSVYIELGSDSSDVTNKAATYCSVGDQELLIQITPQGRDEI
150 160 170 180 190 200 210

220 230 240 250 260 270 280
SLDSAKKAACEFSTDTNTEHOPSNNDLNTTEKRAAERHPKYQGSSVSNLHVEPCGTNTHASSLOHENS
SLDSAKKAACEFSTDTNTEHOPSNNDLNTTEKRAAERHPKYQGSSVSNLHVEPCGTNTHASSLOHENS
220 230 240 250 260 270 280

290 300 310 320 330 340 350 360
SLLLTQDMNVKAEFCNKSQKGLARSOHNRWAGSKETCNDRTTPSTKKVDLNADPLCEKKNWKQLPC
SLLLTQDMNVKAEFCNKSQKGLARSOHNRWAGSKETCNDRTTPSTKKVDLNADPLCEKKNWKQLPC
290 300 310 320 330 340 350 360

370 380 390 400 410 420 430
SENPRDTEVPWITLNSIQKVNWFPSRDELLGSDSDHGESESNKAVADVLDVLEVDYSGSSEKIDLL
SENPRDTEVPWITLNSIQKVNWFPSRDELLGSDSDHGESESNKAVADVLDVLEVDYSGSSEKIDLL
370 380 390 400 410 420 430

440 450 460 470 480 490 500
ASDDEHALICKSERVSHKSVESNIEDKIFGKTYRKASLPNLSHTVTELLIIGAVTTPQIIQERPLTNKLKR
ASDDEHALICKSERVSHKSVESNIEDKIFGKTYRKASLPNLSHTVTELLIIGAVTTPQIIQERPLTNKLKR
440 450 460 470 480 490 500

510 520 530 540 550 560 570
KRRPTSLGLHPEDFIKKADLAVQKTPENINQOTNTEONGQVMNITNSGHENKTKGDSIQNEKNPNLESLEK
KRRPTSLGLHPEDFIKKADLAVQKTPENINQOTNTEONGQVMNITNSGHENKTKGDSIQNEKNPNLESLEK
510 520 530 540 550 560 570

580 590 600 610 620 630 640
ESAFKTKAEPISSSISNWELELNHNSKAPKQNLRRKSTRHHALELVVSRNLSPPNCTELQIDSCSSSE
ESAFKTKAEPISSSISNWELELNHNSKAPKQNLRRKSTRHHALELVVSRNLSPPNCTELQIDSCSSSE
580 590 600 610 620 630 640

```
650 660 670 680 690 700 710 720
EIKKKKYNOMPVRHNRNLQLMGKKEPATCAKSKNKNENOTSKRHSDTTPPELKLITWAPGSFTKCSNTSELKE
650 660 670 680 690 700 710 720
EIKKKKYNOMPVRHNRNLQLMGKKEPATCAKSKNKNENOTSKRHSDTTPPELKLITWAPGSFTKCSNTSELKE
730 740 750 760 770 780 790
FVNPSLPREEKEKLTIVKVSNNAEADPKDMLSGERVLQTERSVESSSISLVPGTYGTQGESISLLEVSTLG
730 740 750 760 770 780 790
FVNPSLPREEKEKLTIVKVSNNAEADPKDMLSGERVLQTERSVESSSISLVPGTYGTQGESISLLEVSTLG
800 810 820 830 840 850 860
KAKTENKCVSQCAAFENPKGLIHGCSKNRNDTEGFKYPLGHEVNHRSRETSIEMEESILDQYLQNTPKVS
800 810 820 830 840 850 860
KAKTENKCVSQCAAFENPKGLIHGCSKNRNDTEGFKYPLGHEVNHRSRETSIEMEESILDQYLQNTPKVS
870 880 890 900 910 920 930
KXQSPALFNPNGNAEECATFSAHSGSLKKQSPKVTFECEQKEENQKKNESNIKPVQTVNITAGFPVVGQKD
870 880 890 900 910 920 930
KXQSPALFNPNGNAEECATFSAHSGSLKKQSPKVTFECEQKEENQKKNESNIKPVQTVNITAGFPVVGQKD
940 950 960 970 980 990 1000
KPDVNAKCSIKGSRFCLSSQFRGNETGLITPNKHGLLQNPYRIPPLFPFKGFVKTKCKKNLLENFEBHSM
940 950 960 970 980 990 1000
KPDVNAKCSIKGSRFCLSSQFRGNETGLITPNKHGLLQNPYRIPPLFPFKGFVKTKCKKNLLENFEBHSM
1010 1020 1030 1040 1050 1060 1070 1080
SPEREMNGENIPSTVSTISGRNIRENVFPGASSNINEVSGSSNINEIGSSDENIQAEIAGNRGPKL
1010 1020 1030 1040 1050 1060 1070 1080
SPEREMNGENIPSTVSTISGRNIRENVFPGASSNINEVSGSSNINEIGSSDENIQAEIAGNRGPKL
1090 1100 1110 1120 1130 1140 1150
NAMLRGLVLOPEVYKQSLPGSKCKHPEIKQKQVEEVVQVNTDFSPYLLSDNLEQPMGSSHASQVCSFETPD
1090 1100 1110 1120 1130 1140 1150
NAMLRGLVLOPEVYKQSLPGSKCKHPEIKQKQVEEVVQVNTDFSPYLLSDNLEQPMGSSHASQVCSFETPD
1160 1170 1180 1190 1200 1210 1220
LDDGEIKEDTSAFENDIKESAVFSKSVORGELSPSPFTTHLAQYRRGAKKLESSENLSEDEELP
1160 1170 1180 1190 1200 1210 1220
LDDGEIKEDTSAFENDIKESAVFSKSVORGELSPSPFTTHLAQYRRGAKKLESSENLSEDEELP
1230 1240 1250 1260 1270 1280 1290
CFQHLLFGKVNPIPQSTHRSTHSTVATECLSKNTEENLLSLKNSLNDCSNOVILAKASQEHHLSEETKCSASLF
1230 1240 1250 1260 1270 1280 1290
CFQHLLFGKVNPIPQSTHRSTHSTVATECLSKNTEENLLSLKNSLNDCSNOVILAKASQEHHLSEETKCSASLF
1300 1310 1320 1330 1340 1350 1360
SSQCELELDTANTQDPFLIGSSKQMHQESQGVGLSDKELVSDDEERTGLEENNQEQSMDSNLGEA
1300 1310 1320 1330 1340 1350 1360
SSQCELELDTANTQDPFLIGSSKQMHQESQGVGLSDKELVSDDEERTGLEENNQEQSMDSNLGEA
1370 1380 1390 1400 1410 1420 1430 1440
ASGCSETSVSDCSGLSQSDILTTQQRTDTHQHNLIKQOEMAELEAVLEOHGSPQNSYPSIISDSALE
1370 1380 1390 1400 1410 1420 1430 1440
ASGCSETSVSDCSGLSQSDILTTQQRTDTHQHNLIKQOEMAELEAVLEOHGSPQNSYPSIISDSALE
1450 1460 1470 1480 1490 1500 1510
DLRNPQSTSEKAVITSQKSEYPISTQNPEGLSADKFEVSADSSSTKNKEPQGVRSPPSKCPSLDRWTMHS
1450 1460 1470 1480 1490 1500 1510
DLRNPQSTSEKAVITSQKSEYPISTQNPEGLSADKFEVSADSSSTKNKEPQGVRSPPSKCPSLDRWTMHS
1520 1530 1540 1550 1560 1570 1580
DLRNPQSTSEKAVITSQKSEYPISTQNPEGLSADKFEVSADSSSTKNKEPQGVRSPPSKCPSLDRWTMHS
```

```
CSGSLQNRNYPQSEELIKVDVVEEQOLBESGPHDLTETSYLPRODLEGTPYLESGISLFSDDPSPDSBDA
1520 1530 1540 1550 1560 1570 1580
CSGSLQNRNYPQSEELIKVDVVEEQOLBESGPHDLTETSYLPRODLEGTPYLESGISLFSDDPSPDSBDA
1590 1600 1610 1620 1630 1640 1650
PESARVGNIPSTSAKVPQKVAESAQAQPAAAHTTDTAGVNAMEESVSREKPELTASTERNKMSVMVSG
1590 1600 1610 1620 1630 1640 1650
PESARVGNIPSTSAKVPQKVAESAQAQPAAAHTTDTAGVNAMEESVSREKPELTASTERNKMSVMVSG
1660 1670 1680 1690 1700 1710 1720
LTPSEFMLVYKFAKHHITLNLITEETHVVMKTDABFVCERTLYKFLGIAGGKVVSYFWVTQSIKERKM
1660 1670 1680 1690 1700 1710 1720
LTPSEFMLVYKFAKHHITLNLITEETHVVMKTDABFVCERTLYKFLGIAGGKVVSYFWVTQSIKERKM
1730 1740 1750 1760 1770 1780 1790 1800
LNEHDFEVRGDIVVNGRNGHQPRAKRESQDRKIFRGLIECCYGFPTNMTDQLEMMVQLCGASVVKELSSFTL
1730 1740 1750 1760 1770 1780 1790 1800
LNEHDFEVRGDIVVNGRNGHQPRAKRESQDRKIFRGLIECCYGFPTNMTDQLEMMVQLCGASVVKELSSFTL
1810 1820 1830 1840 1850 1860 1870 1880
GTGVHPVVVQPDAMTEGDFHAIQMCEAPVVTREWLDSVALYQCCOELDTYLIPOIPHSY
1810 1820 1830 1840 1850 1860 1870 1880
GTGVHPVVVQPDAMTEGDFHAIQMCEAPVVTREWLDSVALYQCCOELDTYLIPOIPHSY
1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
X 10 20 30 40 50 60 70
MDLSALRVEEVQNVINAMQKILEPCICLELIKEPVSTKCDHIFCFKMLKLNKQKGSQCPCKNDITKRS
MDLSALRVEEVQNVINAMQKILEPCICLELIKEPVSTKCDHIFCFKMLKLNKQKGSQCPCKNDITKRS
X 10 20 30 40 50 60 70
LQESTRFSQVLEELKIIICAFQDITGLYANSYFPAKKNNSPEHLKDEVSIIOQSMGYRNRKRLIQSEPEN
LQESTRFSQVLEELKIIICAFQDITGLYANSYFPAKKNNSPEHLKDEVSIIOQSMGYRNRKRLIQSEPEN
150 160 170 180 190 200 210
PSLOETSLSVOLSNLGTVRTLTQKRIQPKTSVYIELGSDSSEDTVNKATYCSVGDOELLIQITPQGTREI
PSLOETSLSVOLSNLGTVRTLTQKRIQPKTSVYIELGSDSSEDTVNKATYCSVGDOELLIQITPQGTREI
150 160 170 180 190 200 210
PSLOETSLSVOLSNLGTVRTLTQKRIQPKTSVYIELGSDSSEDTVNKATYCSVGDOELLIQITPQGTREI
PSLOETSLSVOLSNLGTVRTLTQKRIQPKTSVYIELGSDSSEDTVNKATYCSVGDOELLIQITPQGTREI
220 230 240 250 260 270 280
SIDSAKKAACCFSEDTVTNTHHOPSNNDLNTTEKRAAERHPEKTYQGSVSNLHVEPCGTTNTHASSLOHENS
SIDSAKKAACCFSEDTVTNTHHOPSNNDLNTTEKRAAERHPEKTYQGSVSNLHVEPCGTTNTHASSLOHENS
220 230 240 250 260 270 280
SIDSAKKAACCFSEDTVTNTHHOPSNNDLNTTEKRAAERHPEKTYQGSVSNLHVEPCGTTNTHASSLOHENS
SIDSAKKAACCFSEDTVTNTHHOPSNNDLNTTEKRAAERHPEKTYQGSVSNLHVEPCGTTNTHASSLOHENS
290 300 310 320 330 340 350 360
SILLITKDRMNVKEAFCKNKSQPGIARSOHNRWAGSKETCDNRRTPTSTKKVDLMDADPLCKRKNWKQKLP
SILLITKDRMNVKEAFCKNKSQPGIARSOHNRWAGSKETCDNRRTPTSTKKVDLMDADPLCKRKNWKQKLP
290 300 310 320 330 340 350 360
SILLITKDRMNVKEAFCKNKSQPGIARSOHNRWAGSKETCDNRRTPTSTKKVDLMDADPLCKRKNWKQKLP
SILLITKDRMNVKEAFCKNKSQPGIARSOHNRWAGSKETCDNRRTPTSTKKVDLMDADPLCKRKNWKQKLP
370 380 390 400 410 420 430
SENPRDTEDEVPIITINSIQKVNWFPSRDELGSDSHDGESESNKAVADVLDVINEVDVYSSESSEKIDLL
SENPRDTEDEVPIITINSIQKVNWFPSRDELGSDSHDGESESNKAVADVLDVINEVDVYSSESSEKIDLL
370 380 390 400 410 420 430
SENPRDTEDEVPIITINSIQKVNWFPSRDELGSDSHDGESESNKAVADVLDVINEVDVYSSESSEKIDLL
SENPRDTEDEVPIITINSIQKVNWFPSRDELGSDSHDGESESNKAVADVLDVINEVDVYSSESSEKIDLL
```

2. US-09-982-828-2 (1-1863)

US-09-982-828-2 Sequence 2, Application US/09982828

Initial Score = 1863 Optimized Score = 1863 Significance = 1.73
Residue Identity = 100% Matches = 1863 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

440 450 460 470 480 490 500
 ASDPHALICKSRVSHKSVESNIEDKIFGKTYRKKASLPLNLSHVTENLIIGAFVTEPQIIQRRPLTNKLR
 440 450 460 470 480 490 500
 ASDPHALICKSRVSHKSVESNIEDKIFGKTYRKKASLPLNLSHVTENLIIGAFVTEPQIIQRRPLTNKLR
 510 520 530 540 550 560 570
 KRPTSLGHPDEIKKADIAVQKTPENINGQVMTITNGSHENKTKGDSIQNEKNPNPTESLEK
 510 520 530 540 550 560 570
 KRPTSLGHPDEIKKADIAVQKTPENINGQVMTITNGSHENKTKGDSIQNEKNPNPTESLEK
 580 590 600 610 620 630 640
 ESFAFKTAEPISSISNMELNHNHNSKAPKNRLRKSSTRHIALELVVSNLSPNCTELQIDSCSSSE
 580 590 600 610 620 630 640
 ESFAFKTAEPISSISNMELNHNHNSKAPKNRLRKSSTRHIALELVVSNLSPNCTELQIDSCSSSE
 650 660 670 680 690 700 710 720
 EIKKKYNOMPVRHSRNLQMEGKEPATGAKKNKPNQTSKRHSDTFFPELKLITNAPGFTKCSNTSELKE
 650 660 670 680 690 700 710 720
 EIKKKYNOMPVRHSRNLQMEGKEPATGAKKNKPNQTSKRHSDTFFPELKLITNAPGFTKCSNTSELKE
 730 740 750 760 770 780 790
 FVNPSLPREEKEKLETKVSNNAEDPKDMLSGERVLOTSESVSSISLVPQTDYGTQESISLLEVSTLG
 730 740 750 760 770 780 790
 FVNPSLPREEKEKLETKVSNNAEDPKDMLSGERVLOTSESVSSISLVPQTDYGTQESISLLEVSTLG
 800 810 820 830 840 850 860
 KAKTEPNKCVQCAAFENPKGLIHGCSKONRNDTEGPKYPLGHEVNHRSRTSIEMSELDQYLVQNTFKVS
 800 810 820 830 840 850 860
 KAKTEPNKCVQCAAFENPKGLIHGCSKONRNDTEGPKYPLGHEVNHRSRTSIEMSELDQYLVQNTFKVS
 870 880 890 900 910 920 930
 KRQSFALFSGNAGNAECATFSAHSGSLKKQSPKVPTECEQKEENQKESNIPKQVNTNITAGFPVVGOKD
 870 880 890 900 910 920 930
 KRQSFALFSGNAGNAECATFSAHSGSLKKQSPKVPTECEQKEENQKESNIPKQVNTNITAGFPVVGOKD
 940 950 960 970 980 990 1000
 KPVDNAKCSIKGSRFCLSSQFNGNETGLITPNKHGLLQNPYRIPPLFPKSPVKTKCKNMLEENFEHSM
 940 950 960 970 980 990 1000
 KPVDNAKCSIKGSRFCLSSQFNGNETGLITPNKHGLLQNPYRIPPLFPKSPVKTKCKNMLEENFEHSM
 1010 1020 1030 1040 1050 1060 1070 1080
 SPEREMGNENIPSTVSTISRNIRENVFKGASSNINEVGSSTNEVGSSINEIGSSDENIQABELGRNRGPKL
 1010 1020 1030 1040 1050 1060 1070 1080
 SPEREMGNENIPSTVSTISRNIRENVFKGASSNINEVGSSTNEVGSSINEIGSSDENIQABELGRNRGPKL
 1090 1100 1110 1120 1130 1140 1150
 NAMLRGLVLOPEYKOSLPGSNCKHPEIKKQYEEVVQTYNTDFSPVLIISDNLEQPMGSSHAQVCSSETPDD
 1090 1100 1110 1120 1130 1140 1150
 NAMLRGLVLOPEYKOSLPGSNCKHPEIKKQYEEVVQTYNTDFSPVLIISDNLEQPMGSSHAQVCSSETPDD
 1160 1170 1180 1190 1200 1210 1220
 LLDGGEIKEDTSPAENDIKESSAVFSSKVSQVGLSRSPSPFTHLAQGYRRGAKKLESSEENLSSDEBLP
 1160 1170 1180 1190 1200 1210 1220
 LLDGGEIKEDTSPAENDIKESSAVFSSKVSQVGLSRSPSPFTHLAQGYRRGAKKLESSEENLSSDEBLP
 1230 1240 1250 1260 1270 1280 1290
 CFQHLFGKVNIPSPGSTRHSTVATECLSKNTENLLSKNSLNDSCNQVILAKASQEHLSSETKCSASLF
 1230 1240 1250 1260 1270 1280 1290
 CFQHLFGKVNIPSPGSTRHSTVATECLSKNTENLLSKNSLNDSCNQVILAKASQEHLSSETKCSASLF
 1300 1310 1320 1330 1340 1350 1360
 PSIQETSLSVQSNLGTGVTTLTKQRIQPKQTSVYIELGSDSDSDVTNKAATCSVGVDOELLQITPGOTRDEI
 1300 1310 1320 1330 1340 1350 1360
 PSIQETSLSVQSNLGTGVTTLTKQRIQPKQTSVYIELGSDSDSDVTNKAATCSVGVDOELLQITPGOTRDEI

SSOCSELEDLTANTINTQDPFLIGSSKOMRHOSESQGVGLSDKELVSDDERGTGLENNOEQSMDSNLGEA
 SSOCSELEDLTANTINTQDPFLIGSSKOMRHOSESQGVGLSDKELVSDDERGTGLENNOEQSMDSNLGEA
 1300 1310 1320 1330 1340 1350
 SSOCSELEDLTANTINTQDPFLIGSSKOMRHOSESQGVGLSDKELVSDDERGTGLENNOEQSMDSNLGEA
 1370 1380 1390 1400 1410 1420 1430 1440
 ASCESETSVSEDCSGLSQSDILTTQORDTMOHNLIKQOEMAELEAVLEOHGSPSNSYPSIISDSSALE
 1370 1380 1390 1400 1410 1420 1430 1440
 ASCESETSVSEDCSGLSQSDILTTQORDTMOHNLIKQOEMAELEAVLEOHGSPSNSYPSIISDSSALE
 1450 1460 1470 1480 1490 1500 1510
 DLNRPQSTSEKAVLTSPKSSSEYPISONPEGLSADPFEVSADSTSKNKEPGEVERSSPKCPSLDDRWYHMS
 1450 1460 1470 1480 1490 1500 1510
 DLNRPQSTSEKAVLTSPKSSSEYPISONPEGLSADPFEVSADSTSKNKEPGEVERSSPKCPSLDDRWYHMS
 1520 1530 1540 1550 1560 1570 1580
 CSGLQNRNYPQSEELIKVDVEEQLEESGPHDLTETSYLPRODLEGTPYLESGISLPSDDPESPSDBRA
 1520 1530 1540 1550 1560 1570 1580
 CSGLQNRNYPQSEELIKVDVEEQLEESGPHDLTETSYLPRODLEGTPYLESGISLPSDDPESPSDBRA
 1590 1600 1610 1620 1630 1640 1650
 PESARVGNIPSSSALKVPOLKVAESAQGPAAHTTDTAGYNAMESVSREKPELTASTERNKRMVMVSG
 1590 1600 1610 1620 1630 1640 1650
 PESARVGNIPSSSALKVPOLKVAESAQGPAAHTTDTAGYNAMESVSREKPELTASTERNKRMVMVSG
 1660 1670 1680 1690 1700 1710 1720
 LPEEPFVLVYKFAKHHITLNLITETHTVVMKTDAEFVCERTLKYFLGIAGKVMVSVFWYTQSIKERKM
 1660 1670 1680 1690 1700 1710 1720
 LPEEPFVLVYKFAKHHITLNLITETHTVVMKTDAEFVCERTLKYFLGIAGKVMVSVFWYTQSIKERKM
 1730 1740 1750 1760 1770 1780 1790 1800
 LNEHDFEVDGVDVNGRHHGPKRARSQDKIFRGLIEICYPGFTNMPDQLEMMVQLCGASVVKELSSFTL
 1730 1740 1750 1760 1770 1780 1790 1800
 LNEHDFEVDGVDVNGRHHGPKRARSQDKIFRGLIEICYPGFTNMPDQLEMMVQLCGASVVKELSSFTL
 1810 1820 1830 1840 1850 1860 X
 GTGVHPIVVVQPDWEDNGFHAIGOMCEAPVVVTRWMLDSVALYQCELDYLIPOIHPHY
 1810 1820 1830 1840 1850 1860 X
 GTGVHPIVVVQPDWEDNGFHAIGOMCEAPVVVTRWMLDSVALYQCELDYLIPOIHPHY
 6. US-09-982-828-2 (1-1863)
 US-09-982-828-6 Sequence 6, Application US/09982828
 Initial Score = 1862 Optimized Score = 1862 Significance = 0.00
 Residue Identity = 99% Matches = 1860 Mismatches = 2
 Gaps = 0 Conservative Substitutions = 1
 X 10 20 30 40 50 60 70
 MDLSALRVQVQNVINAMQKILECPICLBLEIKEPVSTKCDHIFCKFCKMLKLNOKKGPSCPLCKNDITKRS
 MDLSALRVQVQNVINAMQKILECPICLBLEIKEPVSTKCDHIFCKFCKMLKLNOKKGPSCPLCKNDITKRS
 X 10 20 30 40 50 60 70
 LQESTFQSVOLBELKIIICAFOLDTCQLEEVANSYFAKKNNSPEHLKDEVSIIQSGVYRNRKRLQSPEN
 LQESTFQSVOLBELKIIICAFOLDTCQLEEVANSYFAKKNNSPEHLKDEVSIIQSGVYRNRKRLQSPEN
 150 160 170 180 190 200 210
 PSI-QETSLSVQSNLGTGVTTLTKQRIQPKQTSVYIELGSDSDSDVTNKAATCSVGVDOELLQITPGOTRDEI
 PSI-QETSLSVQSNLGTGVTTLTKQRIQPKQTSVYIELGSDSDSDVTNKAATCSVGVDOELLQITPGOTRDEI
 150 160 170 180 190 200 210
 PSI-QETSLSVQSNLGTGVTTLTKQRIQPKQTSVYIELGSDSDSDVTNKAATCSVGVDOELLQITPGOTRDEI

220 230 240 250 260 270 280
SLDSAKKAACEFSETDVNTNTEHHQPSNNDLNTTEKRAAERHEPKYQSSVSNLHVEPCGTNTHASSLOHENS
220 230 240 250 260 270 280
SLDSAKKAACEFSETDVNTNTEHHQPSNNDLNTTEKRAAERHEPKYQSSVSNLHVEPCGTNTHASSLOHENS
220 230 240 250 260 270 280
290 300 310 320 330 340 350 360
SLLLTKDRMNYEKAFCNKSQPGGLARQHNRWAGSKETCNDRRTPPSTTEKKVDLNLADPLCRKEKNWKOKLPC
290 300 310 320 330 340 350 360
SLLLTKDRMNYEKAFCNKSQPGGLARQHNRWAGSKETCNDRRTPPSTTEKKVDLNLADPLCRKEKNWKOKLPC
290 300 310 320 330 340 350 360
370 380 390 400 410 420 430
SENPRDTEVPWITLNSIQKNWFSSDELLGSDHGESSENAKVAADVLDVNLNVEVDEYSGSSEKIDLL
370 380 390 400 410 420 430
SENPRDTEVPWITLNSIQKNWFSSDELLGSDHGESSENAKVAADVLDVNLNVEVDEYSGSSEKIDLL
440 450 460 470 480 490 500
ASDPHEALICKSERVHKSVESNIEDKIFGKYRKASLPLNLSHVTENLIIICAFVTEPQIIQERPLTNKLKR
440 450 460 470 480 490 500
ASDPHEALICKSERVHKSVESNIEDKIFGKYRKASLPLNLSHVTENLIIICAFVTEPQIIQERPLTNKLKR
510 520 530 540 550 560 570
KRRPTSGLHPEDFIKKADLAVQKPEMINQGTNTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEK
510 520 530 540 550 560 570
KRRPTSGLHPEDFIKKADLAVQKPEMINQGTNTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEK
580 590 600 610 620 630 640
ESAPKTKAEPISSSISNMELNTHNSKAPKNRLRRKSTRHIIHALELVVSRNLSPNCVTELOIDSCSSSE
580 590 600 610 620 630 640
ESAPKTKAEPISSSISNMELNTHNSKAPKNRLRRKSTRHIIHALELVVSRNLSPNCVTELOIDSCSSSE
650 660 670 680 690 700 710 720
EIKKKKNQMPVHRNRLQLMGEGKEPATGAKSKNPNQTSKRHSDSTFPPELKLITNAPGSKNTSELKE
650 660 670 680 690 700 710 720
EIKKKKNQMPVHRNRLQLMGEGKEPATGAKSKNPNQTSKRHSDSTFPPELKLITNAPGSKNTSELKE
730 740 750 760 770 780 790
FVNPSPREKEKEKLETVKYSNNAEDPKDLMISGERVLQTSRVSSESSISLVPDGTGQTSISLLVSTIG
730 740 750 760 770 780 790
FVNPSPREKEKEKLETVKYSNNAEDPKDLMISGERVLQTSRVSSESSISLVPDGTGQTSISLLVSTIG
800 810 820 830 840 850 860
KAKTEPNKCVSQCAAFENPKGLIHGCSKONRNDTEGPKYPLGHEVNHRSRETSIEMSESLDAQYLQNTFKVS
800 810 820 830 840 850 860
KAKTEPNKCVSQCAAFENPKGLIHGCSKONRNDTEGPKYPLGHEVNHRSRETSIEMSESLDAQYLQNTFKVS
870 880 890 900 910 920 930
KROSFALFSPNPNABECATPSAHSGLSKQSPKVTPECEQKEENQGNKSNIKPVQTVNITAGFPVVGQKD
870 880 890 900 910 920 930
KROSFALFSPNPNABECATPSAHSGLSKQSPKVTPECEQKEENQGNKSNIKPVQTVNITAGFPVVGQKD
940 950 960 970 980 990 1000
KPVDNAKCSIKGSRFCILSSQFRGNETGLITPNKHGLLQNPYRIPPLPKFSFKTKCKKNLLFENFEHSM
940 950 960 970 980 990 1000
KPVDNAKCSIKGSRFCILSSQFRGNETGLITPNKHGLLQNPYRIPPLPKFSFKTKCKKNLLFENFEHSM
1010 1020 1030 1040 1050 1060 1070 1080
SPEREMGNENIPSTVSTISRNIRENVFKGASSNINEVGSSTNEVGSSENEIGSSDENIQAEIGRNRGPKL
1010 1020 1030 1040 1050 1060 1070 1080
SPEREMGNENIPSTVSTISRNIRENVFKGASSNINEVGSSTNEVGSSENEIGSSDENIQAEIGRNRGPKL
1090 1100 1110 1120 1130 1140 1150
GTGVHPITVVVQPDAMTEDNGFHAIGOMCEAPVVTREWLDSVALYOCQELDTYLIQIPHSHY
1090 1100 1110 1120 1130 1140 1150
GTGVHPITVVVQPDAMTEDNGFHAIGOMCEAPVVTREWLDSVALYOCQELDTYLIQIPHSHY

NAMRLGLVLOPEVYKQSLPGSNCKHPETKKOEYEVVQTVNTDFSPYILISNLRQPMGSSHASQVCSETPDD
1090 1100 1110 1120 1130 1140 1150
NAMRLGLVLOPEVYKQSLPGSNCKHPETKKOEYEVVQTVNTDFSPYILISNLRQPMGSSHASQVCSETPDD
1160 1170 1180 1190 1200 1210 1220
LLDDGEIKEDTSPAENDIKESSAVFSKQVSGELSRSPSPETHTHLAQGVRRGAKKLESSEENISSEDEELP
1160 1170 1180 1190 1200 1210 1220
LLDDGEIKEDTSPAENDIKESSAVFSKQVSGELSRSPSPETHTHLAQGVRRGAKKLESSEENISSEDEELP
1230 1240 1250 1260 1270 1280 1290
CFQHLFGKVNIPISQSTRHSTVATECLSKNTEENLLSKNSLNDCCNQVILAKASQEHHLSESTKCSASF
1230 1240 1250 1260 1270 1280 1290
CFQHLFGKVNIPISQSTRHSTVATECLSKNTEENLLSKNSLNDCCNQVILAKASQEHHLSESTKCSASF
1300 1310 1320 1330 1340 1350 1360
SSQCSSELEDLTANTNTQDPFLIGSSKOMRHQSBESQVGLSDKELVSDDEERGTCLENNQBEQSMDSNLGEA
1300 1310 1320 1330 1340 1350 1360
SSQCSSELEDLTANTNTQDPFLIGSSKOMRHQSBESQVGLSDKELVSDDEERGTCLENNQBEQSMDSNLGEA
1370 1380 1390 1400 1410 1420 1430 1440
ASGCSESTSVESDCGLSSQSDILTTQORTMHNLIKLOEAMAELEAVLEHQSGQSPNSVPSIISSSALE
1370 1380 1390 1400 1410 1420 1430 1440
ASGCSESTSVESDCGLSSQSDILTTQORTMHNLIKLOEAMAELEAVLEHQSGQSPNSVPSIISSSALE
1450 1460 1470 1480 1490 1500 1510
DLRNPQOSTSEKAVLTSQKSSEYPISONPEGLSADKEVSDAGSTSKNKEPGVRSRSPSKCPSLDDRWMHS
1450 1460 1470 1480 1490 1500 1510
DLRNPQOSTSEKAVLTSQKSSEYPISONPEGLSADKEVSDAGSTSKNKEPGVRSRSPSKCPSLDDRWMHS
1520 1530 1540 1550 1560 1570 1580
CSGSLQNRNYPSEBILKVVDVBEQQLLESGPHDLTETSYPQLDLEGTPLYESGILFSDDPESDSEDRA
1520 1530 1540 1550 1560 1570 1580
CSGSLQNRNYPSEBILKVVDVBEQQLLESGPHDLTETSYPQLDLEGTPLYESGILFSDDPESDSEDRA
1590 1600 1610 1620 1630 1640 1650
PESARVGNIPSSSALKVPOLKVAESAQSPAAAHITDTAGNAMEESVSREKPELTASTERVNKRMSVMVYSG
1590 1600 1610 1620 1630 1640 1650
PESARVGNIPSSSALKVPOLKVAESAQSPAAAHITDTAGNAMEESVSREKPELTASTERVNKRMSVMVYSG
1660 1670 1680 1690 1700 1710 1720
LTPPEFMLVYKFAKHHITLNTLITETTHVNMKTDAEFVCERTLYFLGIAGGKVVSVFWTQSIKERM
1660 1670 1680 1690 1700 1710 1720
LTPPEFMLVYKFAKHHITLNTLITETTHVNMKTDAEFVCERTLYFLGIAGGKVVSVFWTQSIKERM
1730 1740 1750 1760 1770 1780 1790 1800
LNBHFEVRDGVNGRNHQPKKARSDQRKIFRGLIICCYPGFTNMPTDQLEWMVOLCCASVVKELSSFTL
1730 1740 1750 1760 1770 1780 1790 1800
LNBHFEVRDGVNGRNHQPKKARSDQRKIFRGLIICCYPGFTNMPTDQLEWMVOLCCASVVKELSSFTL
1810 1820 1830 1840 1850 1860 X
GTGVHPITVVVQPDAMTEDNGFHAIGOMCEAPVVTREWLDSVALYOCQELDTYLIQIPHSHY
1810 1820 1830 1840 1850 1860 X
GTGVHPITVVVQPDAMTEDNGFHAIGOMCEAPVVTREWLDSVALYOCQELDTYLIQIPHSHY

> O <
O||O IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seqid4_vs_6.res made by spaul on Fri 19 Mar 104 13:51:34-PST.

Query sequence being compared: US-09-982-828-4 (1-1863)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-982-828-4 (1-1863) with:
File: US09982828.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
R 5-
Q -
U -
E -
N -
C -
E -
S 0-
SCORE 0 207 414 621 828 1035 1242 1449 1656 1863
STDEV

PARAMETERS

Similarity matrix PAM-150 K-tuple 2
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 500
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 1862 Median 1863 Standard Deviation 0.58
Times: CPU 00:00:00.01 Total Elapsed 00:00:00.00

Number of residues: 5589
Number of sequences searched: 3
Number of scores above cutoff: 3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Score	Init.	Opt.
US-09-982-828-4	Sequence 4, Application US	1863	1863	1.73	0
US-09-982-828-2	Sequence 2, Application US	1863	1863	1.73	0

- US-09-982-828-4 Sequence 4, Application US 1863 1863 1863 1.73 0
- US-09-982-828-2 Sequence 2, Application US 1863 1863 1863 1.73 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Sig.	Frame
3. US-09-982-828-6	Sequence 6, Application US	1863	1862	1862	0.00 0

- US-09-982-828-4 (1-1863)
US-09-982-828-4 Sequence 4, Application US/09982828

Initial Score = 1863 Optimized Score = 1863 Significance = 1.73
Residue Identity = 100% Matches = 1863 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X	10	20	30	40	50	60	70
MDLSALRVVEVQVNVINAMOKILPCICLELIKEPVSTKCDHIFCKFCMLKLLNKKQKPGSCPLCKNDITKRS							
MDLSALRVVEVQVNVINAMOKILPCICLELIKEPVSTKCDHIFCKFCMLKLLNKKQKPGSCPLCKNDITKRS							
X	10	20	30	40	50	60	70
LOBSTRESOLVBEILLKIIICAFOLDTGLEYANSYNFAKKNNSPEHLKDEVSIIQSMGYRNRKRLQSEPEN							
LOBSTRESOLVBEILLKIIICAFOLDTGLEYANSYNFAKKNNSPEHLKDEVSIIQSMGYRNRKRLQSEPEN							
X	80	90	100	110	120	130	140
PSLOETSLSVOLSNLGTVRTLRKQRIQPOKTSVYIELGSDSDSDTWNKATYCSVGDQELLOITPQOTRDEI							
PSLOETSLSVOLSNLGTVRTLRKQRIQPOKTSVYIELGSDSDSDTWNKATYCSVGDQELLOITPQOTRDEI							
X	150	160	170	180	190	200	210
SLDSAKKACAFESFETDVTNTEHQPNSNDLNTTEKAAERHPKYOQSSVSNLHVPCGTNTTASSLQHNHS							
SLDSAKKACAFESFETDVTNTEHQPNSNDLNTTEKAAERHPKYOQSSVSNLHVPCGTNTTASSLQHNHS							
X	220	230	240	250	260	270	280
SLLLTKDRNVKAEFCNKSQKPLARSQHNWAGSKETCNDRTSTTEKKVDLNADPLCERKEMNKQKLP							
SLLLTKDRNVKAEFCNKSQKPLARSQHNWAGSKETCNDRTSTTEKKVDLNADPLCERKEMNKQKLP							
X	290	300	310	320	330	340	350
SENPRDTEVPMTLNSSIOKYNWFSRDELLGSDSDSDHGESENAKADVLDVNLNVEVDEYSGSSEKIDLL							
SENPRDTEVPMTLNSSIOKYNWFSRDELLGSDSDSDHGESENAKADVLDVNLNVEVDEYSGSSEKIDLL							
X	370	380	390	400	410	420	430
ASDPHEALICKSERVHKSVEVNIEDKIFGKTYRKASLPNLSHYTENIIIGAFVTEPQIIQERPLTNKLR							
ASDPHEALICKSERVHKSVEVNIEDKIFGKTYRKASLPNLSHYTENIIIGAFVTEPQIIQERPLTNKLR							
X	440	450	460	470	480	490	500
KERPTSGHLHPEDFIKKADLAVOKTEPMINQGTQNGQVNMNITNSGHENKTGDSIQNEKNPNPIESLEK							
KERPTSGHLHPEDFIKKADLAVOKTEPMINQGTQNGQVNMNITNSGHENKTGDSIQNEKNPNPIESLEK							
X	510	520	530	540	550	560	570
ESAFKTKAEPISSSISNMELNINHSKAPKNRLRRKSSSTPHIHALELVSRNLSPPNCTBLQIDSCSSSE							
ESAFKTKAEPISSSISNMELNINHSKAPKNRLRRKSSSTPHIHALELVSRNLSPPNCTBLQIDSCSSSE							
X	580	590	600	610	620	630	640

650	660	670	680	690	700	710	720
EIKKKYINQMPVHSHNNLOIMFGKEPATGAKSNKPNQTSKRHDSDTFPLBKLTNAPGSPFKCNTSELKE							
EIKKKYINQMPVHSHNNLOIMFGKEPATGAKSNKPNQTSKRHDSDTFPLBKLTNAPGSPFKCNTSELKE							
EIKKKYINQMPVHSHNNLOIMFGKEPATGAKSNKPNQTSKRHDSDTFPLBKLTNAPGSPFKCNTSELKE							
650	660	670	680	690	700	710	720
FVNPSLPREKSEKLTWKVSNNAEDPKDMLSGERVLOTSHSVSSSISLVPGDTYGTQBSISLLVSTLIG							
FVNPSLPREKSEKLTWKVSNNAEDPKDMLSGERVLOTSHSVSSSISLVPGDTYGTQBSISLLVSTLIG							
FVNPSLPREKSEKLTWKVSNNAEDPKDMLSGERVLOTSHSVSSSISLVPGDTYGTQBSISLLVSTLIG							
800	810	820	830	840	850	860	
KAKTENKCVSOCAAFENPKGLIHGCSKDNNDTEGFKYPIGHEVNHSHRETSIEMSESDAQVLONTFKVS							
KAKTENKCVSOCAAFENPKGLIHGCSKDNNDTEGFKYPIGHEVNHSHRETSIEMSESDAQVLONTFKVS							
KAKTENKCVSOCAAFENPKGLIHGCSKDNNDTEGFKYPIGHEVNHSHRETSIEMSESDAQVLONTFKVS							
870	880	890	900	910	920	930	
KQSFALFSPNGNAEECATFSAHSGSLKKQSPKTFCEQKEHQKQESNIKPQTVNITAGFPVVGQKD							
KQSFALFSPNGNAEECATFSAHSGSLKKQSPKTFCEQKEHQKQESNIKPQTVNITAGFPVVGQKD							
KQSFALFSPNGNAEECATFSAHSGSLKKQSPKTFCEQKEHQKQESNIKPQTVNITAGFPVVGQKD							
870	880	890	900	910	920	930	
940	950	960	970	980	990	1000	
KQVDNAKCSIKGSRFCLSSOPRGNETGLITPNKHGLLQNPYRIPPLFPFKSVFKTKCKKNLLEENFEHSM							
KQVDNAKCSIKGSRFCLSSOPRGNETGLITPNKHGLLQNPYRIPPLFPFKSVFKTKCKKNLLEENFEHSM							
KQVDNAKCSIKGSRFCLSSOPRGNETGLITPNKHGLLQNPYRIPPLFPFKSVFKTKCKKNLLEENFEHSM							
940	950	960	970	980	990	1000	
1010	1020	1030	1040	1050	1060	1070	1080
SPEREMGMENTPSTVSTSRNNIRENVFKGASSNINEVGSSTNEVGSSEINIEIGSSDENTQAEILGRNRGPKL							
SPEREMGMENTPSTVSTSRNNIRENVFKGASSNINEVGSSTNEVGSSEINIEIGSSDENTQAEILGRNRGPKL							
SPEREMGMENTPSTVSTSRNNIRENVFKGASSNINEVGSSTNEVGSSEINIEIGSSDENTQAEILGRNRGPKL							
1010	1020	1030	1040	1050	1060	1070	1080
1090	1100	1110	1120	1130	1140	1150	
NAMLRLGVLQPEVYKQSLPGSNCKHPETIKQOYEEVQTVNTDPSYLIENDLEQPMGSSHASQVCSPTDD							
NAMLRLGVLQPEVYKQSLPGSNCKHPETIKQOYEEVQTVNTDPSYLIENDLEQPMGSSHASQVCSPTDD							
NAMLRLGVLQPEVYKQSLPGSNCKHPETIKQOYEEVQTVNTDPSYLIENDLEQPMGSSHASQVCSPTDD							
1160	1170	1180	1190	1200	1210	1220	
LLDDGEIKEDTSPANDIKESNAVPSKSVQGEILSRGSPPTHTLQAQYRRGAKKLESSENLSEDEELP							
LLDDGEIKEDTSPANDIKESNAVPSKSVQGEILSRGSPPTHTLQAQYRRGAKKLESSENLSEDEELP							
LLDDGEIKEDTSPANDIKESNAVPSKSVQGEILSRGSPPTHTLQAQYRRGAKKLESSENLSEDEELP							
1230	1240	1250	1260	1270	1280	1290	
CFQHLFGKVNIPSQSTHSTVATECLSKNTENLLSKNSLNCDSNQVILAKASQEHHLSETKCSASLF							
CFQHLFGKVNIPSQSTHSTVATECLSKNTENLLSKNSLNCDSNQVILAKASQEHHLSETKCSASLF							
CFQHLFGKVNIPSQSTHSTVATECLSKNTENLLSKNSLNCDSNQVILAKASQEHHLSETKCSASLF							
1300	1310	1320	1330	1340	1350	1360	
SSQCELEDLTANTNTPDFFLIGSSKOMRSHESQGVGLSDKELVSDDEERGTLERNQOESQMSDNLGEA							
SSQCELEDLTANTNTPDFFLIGSSKOMRSHESQGVGLSDKELVSDDEERGTLERNQOESQMSDNLGEA							
SSQCELEDLTANTNTPDFFLIGSSKOMRSHESQGVGLSDKELVSDDEERGTLERNQOESQMSDNLGEA							
1370	1380	1390	1400	1410	1420	1430	1440
ASGCESETSVSEDCSLSSQSDILTTQORDTMQHNLIKQOEALEAVLUEFHGSPNSYPSIISDSALE							
ASGCESETSVSEDCSLSSQSDILTTQORDTMQHNLIKQOEALEAVLUEFHGSPNSYPSIISDSALE							
ASGCESETSVSEDCSLSSQSDILTTQORDTMQHNLIKQOEALEAVLUEFHGSPNSYPSIISDSALE							
1450	1460	1470	1480	1490	1500	1510	
DLRNPQSTSEKAVITSQKSEYPISONPEGLSADKEVADSDSTSKNKEPQGVERSSPKCPSLDDRWYTHS							
DLRNPQSTSEKAVITSQKSEYPISONPEGLSADKEVADSDSTSKNKEPQGVERSSPKCPSLDDRWYTHS							
DLRNPQSTSEKAVITSQKSEYPISONPEGLSADKEVADSDSTSKNKEPQGVERSSPKCPSLDDRWYTHS							
1520	1530	1540	1550	1560	1570	1580	

2. US-09-982-828-4 (1-1863)
US-09-982-828-2 Sequence 2, Application US/09982828

```
Initial Score      = 1853  Optimized Score = 1863  Significance = 1.73
Residue Identity = 100%  Matches      = 1863  Mismatches = 0
Gaps              = 0    Conservative Substitutions = 0
```

X	10	20	30	40	50	60	70
MDLSALRVEEVQNVINAMOKILEPICLELILKEPVSTKCDHIFCKFCMLKLLNOKKGPSQCLCKNDITKRS							
X	10	20	30	40	50	60	70
MDLSALRVEEVQNVINAMOKILEPICLELILKEPVSTKCDHIFCKFCMLKLLNOKKGPSQCLCKNDITKRS							
80	90	100	110	120	130	140	
LOESTRSOLVIEELLKIIICAFQDGTGLEVANSYNAFKKENSPEHLKDEVSIIQSMGYRNAKXILLQSESPEN							
80	90	100	110	120	130	140	
LOESTRSOLVIEELLKIIICAFQDGTGLEVANSYNAFKKENSPEHLKDEVSIIQSMGYRNAKXILLQSESPEN							
150	160	170	180	190	200	210	
PSLOETSLSVQLSNIGVRLTRTKORIQPKTSVYIELGSDSEDTVNKATYCSVGDOELLOITPQGTTRDEI							
150	160	170	180	190	200	210	
PSLOETSLSVQLSNIGVRLTRTKORIQPKTSVYIELGSDSEDTVNKATYCSVGDOELLOITPQGTTRDEI							
220	230	240	250	260	270	280	
SLDSAXKAAECFSETDVTNTEHHOPSNNDLNTTEKRAAERPEKYQGSVSNLHVEPCGTNTHASSILOHENS							
220	230	240	250	260	270	280	
SLDSAXKAAECFSETDVTNTEHHOPSNNDLNTTEKRAAERPEKYQGSVSNLHVEPCGTNTHASSILOHENS							
290	300	310	320	330	340	350	360
SLLLTKORMNVKAEAFCKNSKOPGLARSOHNNWAGSKETCNDRRTPSTPEKKVDLNADPLCERKEWNKQKLPC							
290	300	310	320	330	340	350	360
SLLLTKORMNVKAEAFCKNSKOPGLARSOHNNWAGSKETCNDRRTPSTPEKKVDLNADPLCERKEWNKQKLPC							
370	380	390	400	410	420	430	
SENPRDTEVPWILLNSSIOCKYNEWFSRDEILGSDDDSHDGESESNKAVDVLVINEVEDEYSGSSEKIDLL							
370	380	390	400	410	420	430	
SENPRDTEVPWILLNSSIOCKYNEWFSRDEILGSDDDSHDGESESNKAVDVLVINEVEDEYSGSSEKIDLL							

440 450 460 470 480 490 500
ASDPEALICKSERVHKSVEISNEDKIFGKTYRKASLPNLSHVTENLIIGAFVTEPQIIQERELTNKLKR
ASDPEALICKSERVHKSVEISNEDKIFGKTYRKASLPNLSHVTENLIIGAFVTEPQIIQERELTNKLKR
440 450 460 470 480 490 500
510 520 530 540 550 560 570
KRRPTSGLHPEDFIKADLAVOKTPEMINOGTQTEQGVWNIITNSGHENKTGDSIONENKPNPIESLEK
KRRPTSGLHPEDFIKADLAVOKTPEMINOGTQTEQGVWNIITNSGHENKTGDSIONENKPNPIESLEK
510 520 530 540 550 560 570
580 590 600 610 620 630 640
ESAFKTAEPISSSISNMELNINHSKAPKNRURRSSTRHIALELVVSRNLSPPNCTELQIDSCSSSE
ESAFKTAEPISSSISNMELNINHSKAPKNRURRSSTRHIALELVVSRNLSPPNCTELQIDSCSSSE
580 590 600 610 620 630 640
650 660 670 680 690 700 710 720
EIKKKYQMPVRHSRNLOIMEGKEPATGAKSKNPNQTSKRHSDTFFPELKLTNAPGSFTKCSNTSELKE
EIKKKYQMPVRHSRNLOIMEGKEPATGAKSKNPNQTSKRHSDTFFPELKLTNAPGSFTKCSNTSELKE
650 660 670 680 690 700 710 720
730 740 750 760 770 780 790
FVNPSPREEKEKLETVKUSNNAEDPKDMLSGERVLOTERSVESSISLVPGTDTGTQBSISLLEVSTIG
FVNPSPREEKEKLETVKUSNNAEDPKDMLSGERVLOTERSVESSISLVPGTDTGTQBSISLLEVSTIG
730 740 750 760 770 780 790
800 810 820 830 840 850 860
KAKTEPNKVCYOCAPENPKGLIHGCKDNNDTEGFKYPLGHEVNHRSRSTSIEMSESEDAQYLQNTFKVS
KAKTEPNKVCYOCAPENPKGLIHGCKDNNDTEGFKYPLGHEVNHRSRSTSIEMSESEDAQYLQNTFKVS
800 810 820 830 840 850 860
870 880 890 900 910 920 930
KROSFALFSPGNAEECATFSAHSGSLKKOSPKVTECEQKEENQKNESNIRKPVQTNITAGFPVVGQKD
KROSFALFSPGNAEECATFSAHSGSLKKOSPKVTECEQKEENQKNESNIRKPVQTNITAGFPVVGQKD
870 880 890 900 910 920 930
940 950 960 970 980 990 1000
KPDVNAKCSIKGSRFCLSSQFRNETGLTPNKHGLLQNPYRIPPLPIKSFVKTKCKXNLLFENFEHSM
KPDVNAKCSIKGSRFCLSSQFRNETGLTPNKHGLLQNPYRIPPLPIKSFVKTKCKXNLLFENFEHSM
940 950 960 970 980 990 1000
1010 1020 1030 1040 1050 1060 1070 1080
SPEREMGNIPSTVSTISRNIRENVFKGASSNINEVSGSTNEVGSSINEIGSSDENIOAELGRNRGPKL
SPEREMGNIPSTVSTISRNIRENVFKGASSNINEVSGSTNEVGSSINEIGSSDENIOAELGRNRGPKL
1010 1020 1030 1040 1050 1060 1070 1080
1090 1100 1110 1120 1130 1140 1150
NAMLRLGLVQPEVYKQSLPGSNCKHPRIKQOEVEVQVNTDPSPLYISDNLEQPMGSSHASQVCSSETDD
NAMLRLGLVQPEVYKQSLPGSNCKHPRIKQOEVEVQVNTDPSPLYISDNLEQPMGSSHASQVCSSETDD
1090 1100 1110 1120 1130 1140 1150
1160 1170 1180 1190 1200 1210 1220
LLDDGEIKEDTSPAENDIKESSAVFSKVGELSRSPFTHTHLAQGYRRGAKKLESSEENLSSEDEELP
LLDDGEIKEDTSPAENDIKESSAVFSKVGELSRSPFTHTHLAQGYRRGAKKLESSEENLSSEDEELP
1160 1170 1180 1190 1200 1210 1220
1230 1240 1250 1260 1270 1280 1290
CFOHLFGKVNIPSPQSTRSTVATECLSKNTENLLSKNLSNDCSNQVILAKASQEHLSSETKCSASLF
CFOHLFGKVNIPSPQSTRSTVATECLSKNTENLLSKNLSNDCSNQVILAKASQEHLSSETKCSASLF
1230 1240 1250 1260 1270 1280 1290
1300 1310 1320 1330 1340 1350 1360

SSQCELEDLTANTNTQDPFLIGSKOMRHQSOVGCLSKDELVSDDEERGTLLENNQEQSMDNLGEA
SSQCELEDLTANTNTQDPFLIGSKOMRHQSOVGCLSKDELVSDDEERGTLLENNQEQSMDNLGEA
1300 1310 1320 1330 1340 1350 1360
1370 1380 1390 1400 1410 1420 1430 1440
ASGCESETSVSEDCSLSSQSDILTTQORDTMOHNLKIQOEEMAELEAVLEHOGSQSPNSYPSIISDSALE
ASGCESETSVSEDCSLSSQSDILTTQORDTMOHNLKIQOEEMAELEAVLEHOGSQSPNSYPSIISDSALE
1370 1380 1390 1400 1410 1420 1430 1440
1450 1460 1470 1480 1490 1500 1510
DLRNPQSTSEKAVLTISOKSEYPISONPEGLSADKFEVSADSTSKNKEPGRSSPSKPCSLDDRWYMS
DLRNPQSTSEKAVLTISOKSEYPISONPEGLSADKFEVSADSTSKNKEPGRSSPSKPCSLDDRWYMS
1450 1460 1470 1480 1490 1500 1510
1520 1530 1540 1550 1560 1570 1580
CSGSLQNRNYPSEBELIKVVDVEEQLEESGFHDLTETSYLPRODLEGTPLYESGISLFSDDPSDEDR
CSGSLQNRNYPSEBELIKVVDVEEQLEESGFHDLTETSYLPRODLEGTPLYESGISLFSDDPSDEDR
1520 1530 1540 1550 1560 1570 1580
1590 1600 1610 1620 1630 1640 1650
PESARVGNIPSSSTSAKVPOLKVAESAQGPAAHTTDTAGYNAMESVSREKPELTASTERNKRMMSVVS
PESARVGNIPSSSTSAKVPOLKVAESAQGPAAHTTDTAGYNAMESVSREKPELTASTERNKRMMSVVS
1590 1600 1610 1620 1630 1640 1650
1660 1670 1680 1690 1700 1710 1720
LTPPEFMLVYKFAKHHITLNLITEETTHVWKTDAEFVCERTLKYLFIAGGKVVSVFWVTQSIKEROM
LTPPEFMLVYKFAKHHITLNLITEETTHVWKTDAEFVCERTLKYLFIAGGKVVSVFWVTQSIKEROM
1660 1670 1680 1690 1700 1710 1720
1730 1740 1750 1760 1770 1780 1790 1800
LNEHDFEVRDGVNVRNHQPKRAESQDRKIFRGLIEICCYGPFNTMPTQLEMMVOLCCASVVKELSSFTL
LNEHDFEVRDGVNVRNHQPKRAESQDRKIFRGLIEICCYGPFNTMPTQLEMMVOLCCASVVKELSSFTL
1730 1740 1750 1760 1770 1780 1790 1800
1810 1820 1830 1840 1850 1860 X
GTGVHPITVVVQPDADWEDNFGHAIQOMCEAPVVTREWLDLSVALYQOEELDTYLIPOIPSHY
GTGVHPITVVVQPDADWEDNFGHAIQOMCEAPVVTREWLDLSVALYQOEELDTYLIPOIPSHY
1810 1820 1830 1840 1850 1860 X
X 10 20 30 40 50 60 70
MDLSALREVEQVNVINAMQKILECPICLELIKEPVSTKCDHIFCKEMLKLNQKKGPSOCLCKNDITKRS
MDLSALREVEQVNVINAMQKILECPICLELIKEPVSTKCDHIFCKEMLKLNQKKGPSOCLCKNDITKRS
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
LQESTRFSQVLELLKIIICAFOLDTGLEVANSYNFAKKENNSPEHLKDEVSIIQSMGYNRKRLKLSPEEN
LQESTRFSQVLELLKIIICAFOLDTGLEVANSYNFAKKENNSPEHLKDEVSIIQSMGYNRKRLKLSPEEN
80 90 100 110 120 130 140
150 160 170 180 190 200 210
PSIQETSLSVQSLNLTGVTATLTQKRIQPKQTSVYIELGSDSDSTVNKATYCSVGOELQITPGOTRDEI
PSIQETSLSVQSLNLTGVTATLTQKRIQPKQTSVYIELGSDSDSTVNKATYCSVGOELQITPGOTRDEI
150 160 170 180 190 200 210

3. US-09-982-828-4 (1-1863)

US-09-982-828-6 Sequence 6, Application US/09982828

Initial Score = 1862 Optimized Score = 1862 Significance = 0.00
Residue Identity = 99% Matches = 1860 Mismatches = 2
Gaps = 0 Conservative Substitutions = 1

X 10 20 30 40 50 60 70
MDLSALREVEQVNVINAMQKILECPICLELIKEPVSTKCDHIFCKEMLKLNQKKGPSOCLCKNDITKRS
MDLSALREVEQVNVINAMQKILECPICLELIKEPVSTKCDHIFCKEMLKLNQKKGPSOCLCKNDITKRS
X 10 20 30 40 50 60 70
80 90 100 110 120 130 140
LQESTRFSQVLELLKIIICAFOLDTGLEVANSYNFAKKENNSPEHLKDEVSIIQSMGYNRKRLKLSPEEN
LQESTRFSQVLELLKIIICAFOLDTGLEVANSYNFAKKENNSPEHLKDEVSIIQSMGYNRKRLKLSPEEN
80 90 100 110 120 130 140
150 160 170 180 190 200 210
PSIQETSLSVQSLNLTGVTATLTQKRIQPKQTSVYIELGSDSDSTVNKATYCSVGOELQITPGOTRDEI
PSIQETSLSVQSLNLTGVTATLTQKRIQPKQTSVYIELGSDSDSTVNKATYCSVGOELQITPGOTRDEI
150 160 170 180 190 200 210

220	230	240	250	260	270	280
SIDS	AKAACE	SETDVT	TEHQ	SNNDL	NTTEK	RAAERPEKYQGS
220	230	240	250	260	270	280
SIDS	AKAACE	SETDVT	TEHQ	SNNDL	NTTEK	RAAERPEKYQGS
290	300	310	320	330	340	350
SILL	TKDR	MVKA	EFCN	KSGO	GLAR	SOHNRWAGSKETC
290	300	310	320	330	340	350
SILL	TKDR	MVKA	EFCN	KSGO	GLAR	SOHNRWAGSKETC
320	330	340	350	360	370	380
SEN	PR	TE	DV	PW	IT	LNSSIQK
320	330	340	350	360	370	380
SEN	PR	TE	DV	PW	IT	LNSSIQK
420	430	440	450	460	470	480
ASD	PH	EAL	ICK	SER	VH	SKSVES
420	430	440	450	460	470	480
ASD	PH	EAL	ICK	SER	VH	SKSVES
520	530	540	550	560	570	580
KRP	TS	G	L	H	P	E
520	530	540	550	560	570	580
KRP	TS	G	L	H	P	E
620	630	640	650	660	670	680
ES	AF	TK	AE	P	IS	SS
620	630	640	650	660	670	680
ES	AF	TK	AE	P	IS	SS
720	730	740	750	760	770	780
FV	NP	SL	PRE	E	E	K
720	730	740	750	760	770	780
FV	NP	SL	PRE	E	E	K
820	830	840	850	860	870	880
K	A	K	T	E	P	N
820	830	840	850	860	870	880
K	A	K	T	E	P	N
920	930	940	950	960	970	980
K	R	Q	F	A	L	F
920	930	940	950	960	970	980
K	R	Q	F	A	L	F
1020	1030	1040	1050	1060	1070	1080
S	P	E	R	M	G	N
1020	1030	1040	1050	1060	1070	1080
S	P	E	R	M	G	N
1120	1130	1140	1150	1160	1170	1180
1090	1100	1110	1120	1130	1140	1150